

Bioconductor Developers' Forum
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DataFrame/DFrame

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Concrete class vs virtual class

Concrete class: can be instantiated

```
> setClass("C", slots=c(stuff="ANY"))  
> c <- new("C")
```

Virtual class: cannot be instantiated

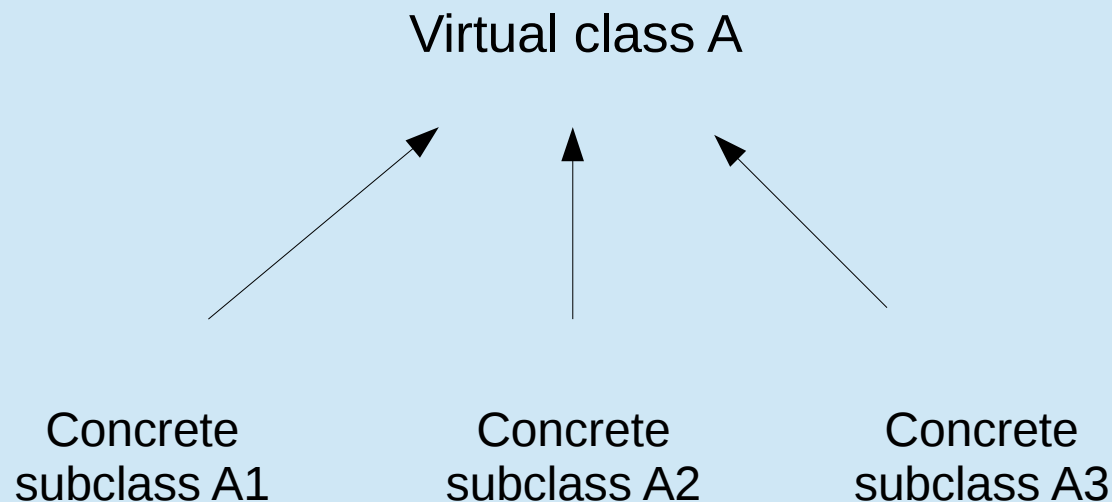
```
> setClass("V", contains="VIRTUAL", slots=c(stuff="ANY"))  
> v <- new("V")  
Error in new("V") :  
  trying to generate an object from a virtual class ("V")
```

When to use a virtual class

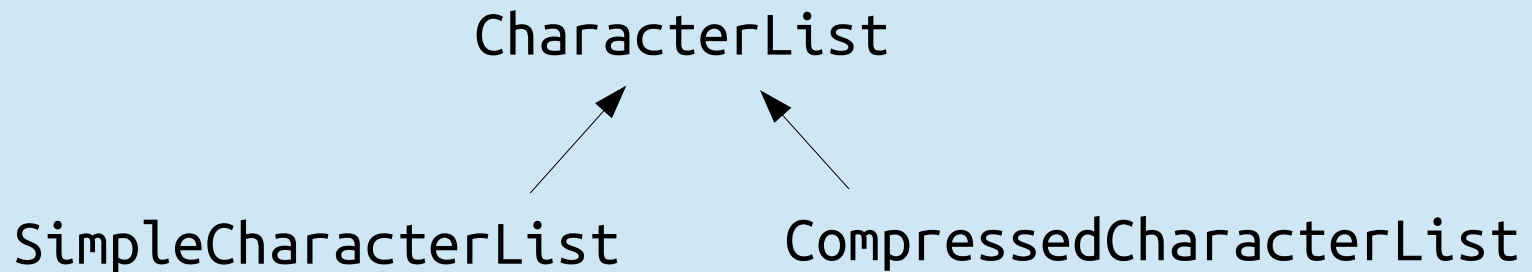
Typically when we want to support more than one implementation of the same “concept”.

The virtual class represents the concept.

Each concrete subclass implements the concept.



Examples of virtual classes in Bioconductor



```
> x1 <- CharacterList(letters[1:5], c(NA, "foo"))
```

```
> x1
```

```
CharacterList of length 2
```

```
[[1]] a b c d e
```

```
[[2]] <NA> foo
```

```
> class(x1)
```

```
[1] "CompressedCharacterList"
```

```
attr(,"package")
```

```
[1] "IRanges"
```

```
> x2 <- CharacterList(letters[1:5], c(NA, "foo"), compress=FALSE)
```

```
> x2
```

```
CharacterList of length 2
```

```
[[1]] a b c d e
```

```
[[2]] <NA> foo
```

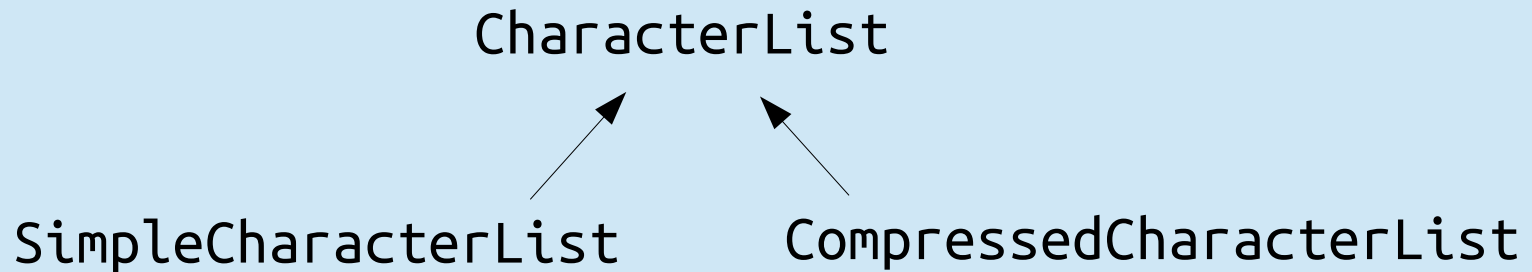
```
> class(x2)
```

```
[1] "SimpleCharacterList"
```

```
attr(,"package")
```

```
[1] "IRanges"
```

2 different CharacterList implementations



```
> getSlots("SimpleCharacterList")
  elementType      elementMetadata      metadata      listData
  "character" "DataTable_OR_NULL"      "list"       "list"

> getSlots("CompressedCharacterList")
  elementType      elementMetadata      metadata      unlistData
  "character" "DataTable_OR_NULL"      "list"       "ANY"
  partitioning
  "PartitioningByEnd"
```

Data-frame-like containers

DataFrame

```
> getSlots("DataFrame")
      rownames          nrows      listData      elementType
"character_OR_NULL"  "integer"    "list"      "character"
      elementMetadata  metadata
"DataTable_OR_NULL"  "list"
```

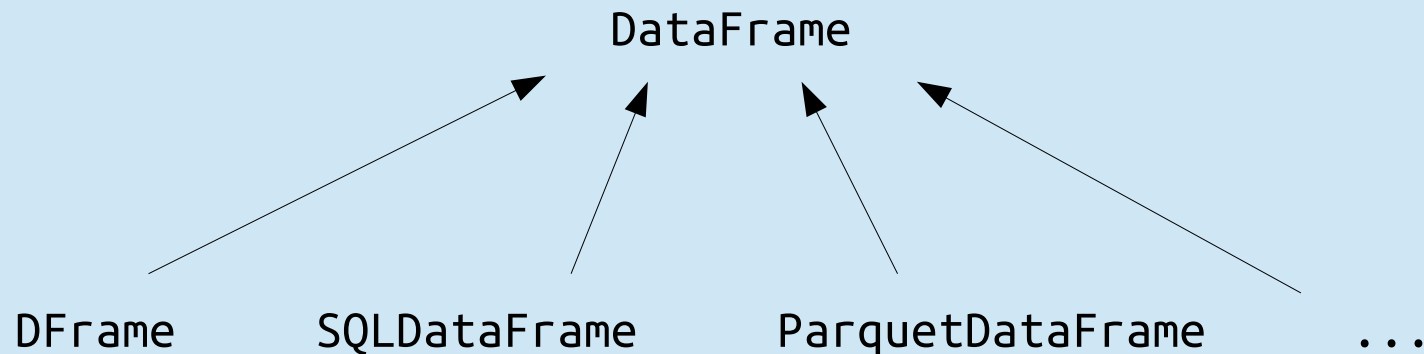
- The columns are stored in an ordinary list (`listData` slot).

SQLDataFrame (work-in-progress)

- Qian Liu, <https://github.com/Bioconductor/SQLDataFrame>
- The data is in an SQL database
- Ideally, we'd like to be able to use an SQLDataFrame object everywhere a DataFrame is expected e.g. for the metadata columns of a Vector derivative:

```
> mcols(x) <- SQLDataFrame(...) # should work
```

The virtual class approach



- DataFrame becomes a virtual class with no slots
- DFrame replaces the original DataFrame (in-memory representation)
- Other DataFrame derivatives implement on-disk representations
- They all support the DataFrame API (`dim`, `nrow`, `ncol`, `[`, `[[`, etc...) possibly with some restrictions (e.g. `[[<-`) for some of the derivatives
- They all should be usable where a DataFrame is expected
- `as(DF, "DFrame")` becomes the standard idiom to load the data in memory

Other benefits

Some methods can be defined at the level of the virtual class:

```
setMethod("dim", "DataFrame", function(x) c(nrow(x), ncol(x)))  
setMethod("length", "DataFrame", function(x) ncol(x))  
setMethod("dimnames", "DataFrame", function(x) c(rownames(x), colnames(x)))  
etc...
```

→ avoids code duplication across the DataFrame derivatives.

Work in progress

- DFrame added to the devel version of S4Vectors in August
- DataFrame() constructor and as(x, "DataFrame") now return an object of class DFrame
- DFrame objects are displayed as being DataFrame object (they are, is())
- Change is transparent for the end user
- Mostly transparent to the developers (use is(x, "DataFrame") rather than class(x) == "DataFrame")
- There is more to complete the DataFrame-to-DFrame migration

Thanks!

Questions?